

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 30, 2002, 11:42:59 ; Search time 1785.4 Seconds
(without alignments)
7735.809 Million cell updates/sec

Title: US-09-733-507-3
Perfect score: 660

Sequence: 1 acgtatagcagctacggag.....gaagtacgaaattgcacaga 660

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

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30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description

1	660	100.0	660	6	AX008793	Sequence
2	658.4	99.8	856	8	ATU94772	Arabidopsis
3	656.8	99.5	904	6	AX008791	Sequence
4	364	55.2	443	6	AX008794	Sequence
5	349.4	52.9	1240	8	AF079587	Arabidops
6	349.4	52.9	98374	8	AC003040	Arabidops
7	342.4	51.9	377	6	AX008795	Sequence
8	92.6	14.0	7218	6	166494	Sequence 14
9	75	11.4	927	8	AB029483	Pisum sat
10	72.4	11.0	804	6	AX008805	Sequence
11	72.4	11.0	804	6	CRJ002173	Chenopodi
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13	67.4	10.2	286584	2	AC091428	Mus muscu
14	63.6	9.6	236962	2	AL606742	Mus muscu
15	63.4	9.6	223547	2	AL611963	Mus muscu
16	63.4	9.6	231122	2	AC090480	Mus muscu
17	63.2	9.6	205638	2	AC040927	Mus muscu
18	63	9.5	223828	2	AC098731	Mus muscu
19	62.4	9.5	201395	10	AC091250	Mus muscu
20	62	9.4	111345	9	AL445531	Human DNA
21	61.8	9.4	157848	9	AC079763	Homo sapi
22	61.6	9.3	63739	2	AC102458	Mus muscu
23	61.6	9.3	203606	2	AL645990	Mus muscu
24	61.4	9.3	175562	9	AP002833	Homo sapi
25	61.2	9.3	588	8	ATH301558	Arabidops
26	61.2	9.3	642	6	AC008798	Sequence
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41	60	9.1	179149	9	AC009785	Homo sapi
42	60	9.1	252957	2	AC105705	Rattus no
43	59.8	9.1	153588	9	AC010533	Homo sapi
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45	59.8	9.1	194070	2	AL663075	Mus muscu

ALIGNMENTS

RESULT	1	AX008793	Sequence	3 from Patent	660 bp	DNA	linear	PAT 06-SEP-2000
LOCUS	AX008793	Sequence	3 from Patent	WO9964599				
DEFINITION	AX008793	Sequence	3 from Patent	WO9964599				
ACCESSION	AX008793	Sequence	3 from Patent	WO9964599				
VERSION	AX008793.1	GI:9996257						
KEYWORDS	thale cress.							
SOURCE	Arabidopsis thaliana							
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.							
REFERENCE	1 (bases 1 to 660)							
AUTHORS	Fowke, L.C., Wang, H. and Crosby, W.L.							
TITLE	Cyclin-dependent kinase inhibitors as plant growth regulators							
JOURNAL	Patent: WO 9964599-A 3 16-DEC-1999;							
	POWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD							
	(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV							
	SASKATCHEWAN TECHNOLOGIES (CA)							
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source	1..660							
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	/db_xref="taxon:3702"							

TITLE	Direct Submission
JOURNAL	Submitted (20-MAR-1997) Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada
FEATURES	Location/Qualifiers
source	1..856
gene	/organism="Arabidopsis thaliana" /strain="Columbia" /db_xref="taxon:3702"
CDS	1..856 7..582 /gene="ICK1" /gene="ICK1" /codon_start=1 /product="cyclin-dependent kinase inhibitor protein" /protein_id="AAC49698.1" /db_xref="GI:2052502" /translation="MVRKYRKAKGIIVEAGSVSTMQRRIYVRSEKSSSVVVGDNVSSSCSGSNKKELIHLEEDKDGDTSTYRRGTRKLCENLRPEKEELSKS MENVSSSEFSAVKSLDCCSGRKTMEETVAEEBKAKLMTTEPTSEIDFFVEAE KOLKEFKKKYNDFEKEPLEGRYEWVLE"
BASE COUNT	292 a 92 c 225 g 247 t
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Best Local Similarity	99.8%; Pred. No. 1.4e-120;
Matches 659; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY 1	acgtatatgacgtacgagcgaggaattgtttatgttagatcggaataatcaagctct 60
Db 61	ACGTATATGACGCTACGAGCGCGGAGAAATGCTTTATGTTAGTCGGAATAATCAAGCTCT 120
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Db 121	GTCTCCGTCGTCGGTGATAATGGAGTTTTCGTCGTCCTTGTAGTGAAGCAATGAATAAAG 180
QY 121	aagaagaataatacatctgagaggaagataaagaatggtgaacatgaacgtgcagc 180
Db 181	ANGAAGAATAATTAATACATCTGGAGGAGGAAGATAAAGTGTGACACTGAACGTCGACG 240
QY 181	tatcgacgggttcagaaagagaagctttttgaaactctgagagggaggagaagaagaa 240
Db 241	TATCGACGGGTACCAAGAGGAAAGCTTTGTGAAAATCTGAGAGAGGAGGAGAAAGAA 300
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Db 301	TTAAGTAATCCATGAGAAATTTATCATCGGAATTTGAATCGGCGGTAAAGAAATCGTTA 360
QY 301	gattgttctgttagcgggaggaacacatgagagagacggtgacgcgagggaggagag 360
Db 361	GATTCTTTTGTAGCGGAGGAAAAACCATGAGGAGACGCTGACGCGGAGGAGGAGGAG 420
QY 361	aagcggaatttgatgcgcgagatcccaacggaatcggaataatcggaatttttctggaa 420
Db 421	AAGCGGAATTTGATGACGGAGATGCCAACGGAATTCGGAATTTTGTGGAATTTTGTGGA 480
QY 421	gctgagaacaactcaagaagaaattcaagaagaatcacaattctgatttcgagaagag 480
Db 481	GCTGAGAAAAACAATCAAGAAAAAATTCAGAGAGAAATTCAGATTCGAGAGAGAGAG 540
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Db 601	TGTTTTTTTTTTTACCTTTTGTAGATTTTAAATTTTCAGGGAATAAGTTAATTTATT 660
QY 601	ttgatttggaaataataagattttagaggaatgttttttagaagtcagaaattgcacaga 660
Db 661	TTGATTTGGAATAATAAGATTTCAGGAGGAATGTTTTTAGAAGTACGAATTCACAGA 720

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Best Local Similarity	100.0%;	Pred. No. 6.8e-121;		
Matches 660; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db 1	ACGTATATGACGCTACGAGCGCGGAGAAATGCTTTATGTTAGTCGGAATAATCAAGCTCT 60			
QY 61	gtctcgtcgtcggtgataatggaggttcgtctgtctgttagtggaaagaataataag 120			
Db 61	GTCTCCGTCGTCGGTGATAATGGAGTTTCGTCGTCCTTGTAGTGAAGCAATGAATAAAG 120			
QY 121	aagaagaataatacatctgagaggaagataaagaatggtgaacatgaacgtgcagc 180			
Db 121	AAGAAAGAATAATACATCTGGAGGAGGAAGATAAAGATGCTGACACTGAACGTCGACG 180			
QY - 181	tatcgacgggttacgaagagaagctttttgaaatctgagagaggaggaagaagaagaa 240			
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Db 241	TTAAGTAAATCCATGAGAAATTAATCATCGGAATTGAATCGCGGTTAAAGATCGTTA 300			
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Db 301	GATTGTGTTGTAGCGGAGGAAAAACGATGAGGAGACGCTGACGCGGAGGAGGAGGAG 360			
QY 361	aagcggaatttgatgcgcgagatgccaaacggaatcggaattttttgttgaa 420			
Db 361	AAGCGGAATTTGATGACGGAGATGCCAACGGAATCGGAAATTTGAGATTTTTCGGA 420			
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QY 601	ttgatttggaaataaagattttagaggaatgttttttagaagtcagaaattgcacaga 660			
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RESULT	2
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LOCUS	856 bp mRNA linear PLN 29-APR-1997
DEFINITION	Arabidopsis thaliana cyclin-dependent kinase inhibitor protein
ACCESSION	U94772
VERSION	U94772.1 GI:2052501
KEYWORDS	thale cress.
SOURCE	Arabidopsis thaliana
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 856)
REFERENCE	Wang, H., Fowke, L.C. and Crosby, W.L.
AUTHORS	Nature 386 (6624), 451-452 (1997)
JOURNAL	97242401
MEDLINE	
REFERENCE	2 (bases 1 to 856)
AUTHORS	Wang, H., Fowke, L.C. and Crosby, W.L.

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RESULT 3
LOCUS AX008791 904 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 1 from Patent WO9964599.
ACCESSION AX008791
VERSION AX008791.1 GI:9996255
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 904)
Fowke,L.C., Wang,H. and Crosby,W.L.
Cyclin-dependent kinase inhibitors as plant growth regulators
Patent: WO 9964599-A 16-DEC-1999;
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
SASKATCHEWAN TECHNOLOGIES (CA)
SASKATCHEWAN TECHNOLOGIES (CA)
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KOLKEKFKKYNFDEKPLEKRYEWKLE"
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Best Local Similarity 99.7%; Pred. No. 2.9e-120;
Matches 658; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 acgtatagcagctacgagcgcggagaatttttatgttagtcggaataatcaagctct 60
Db 109 ACGTATATGCACTACGCGAGCGGAGAATTTTATGTATGATCGGAAAAATCAAGCTCT 168
QY 61 gtctccgtcgctgataatggaggttcgtcgctctttagtgaagcaatgaataaag 120
Db 169 GTCTCCGTCGTCGTGATATGAGTTTCGTCGCTCTGTAGTGAAGCAATGAATATAG 228
QY 121 aagaaagaattatcatctgtgagaggagaataaagatggtgacactgaaactcgacg 180
Db 229 AAGAAAGAATTATATACATCTGGAGGAGGAGATAAAGATGTTGACACTGAAACGTCGACG 288
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Db 289 TATCGACGGGTGACGACGAGGAAGCTTTTGAAATCTGAGAGGAGGAGGAGAAAGAGAA 348
QY 241 ttaagtaaatcattgaggaattattcatcggaattttgaatcgcggtttaaagaatcgta 300
Db 349 TTAAGTAAATCCATGAGAAATTAATTCGGAATTGGAATTCGCGGTTAAGATTCGTTA 408
QY 301 gattgtgttctacgggaggaagaaacatgagagagcgttcgacggcgagagagagag 360
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QY 361 aagcgaaattgatgcgagatgccaacggaatcgaaattgaagatttttttggtaa 420
Db 469 AAGCGGAAATGATGACGGAGATGCCAACCGGAATCGGAAATGGAATGGAATTTTGTGGAA 528
QY 421 gctgagaacaactcaagaaaaattcaagaagaagtacaaatttcgatttcgagaagag 480
Db 529 GCTGAGAAACAACCTCAAGAAAAAATTCAGAGGAAGTACAAATTCGATTTCGAGAGGAG 588
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QY 601 ttgatttggaaataaagatttttagggaggaatgttttttagaagtacgaattgcacga 660
Db 709 TTGATTTCGAAATATAAGATTGTAGGAGSANTGTTTTTAGAAGTACGAAATGCACAGA 768
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LOCUS AX008794
DEFINITION Sequence 4 from Patent WO9964599.
ACCESSION AX008794
VERSION AX008794.1 GI:9996258
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 443)
Fowke,L.C., Wang,H. and Crosby,W.L.
Cyclin-dependent kinase inhibitors as plant growth regulators
Patent: WO 9964599-A 16-DEC-1999;
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
SASKATCHEWAN TECHNOLOGIES (CA)
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Best Local Similarity 100.0%; Pred. No. 2.4e-62;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 atggagaatttcatcgcgaatttgaaatcgcggttaaagaatcgttagattgttgtgt 312
Db 80 ATGGAGAATTATTCATCGGAATTTGAATCGCGGTTAAAGAATCGTTAGATTGTGTGT 139
QY 313 agcgggagaaaacgatggagagacggtgacgcggagagagaggaagcaaaaattg 372
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QY 373 atgcaggagatgcgaacggaatcggaattttttgtggaagctgagaacaa 432
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Db 260 CTCRAAGAAAATTCAGAGAAGTACAAATTCGATTTTCGAGAAGGAGAGGCCATTAGAA 319
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AF079587
LOCUS AF079587 1240 bp DNA linear PLN 07-SEP-1998
DEFINITION Arabidopsis thaliana cyclin-dependent kinase inhibitor (ICK1) gene, complete cds.
ACCESSION AF079587
VERSION AF079587.1 GI:3550261
KEYWORDS thale cress.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE Wang, H., Qi, Q., Schorr, P., Cutler, A. J., Crosby, W. L. and Fowke, L. C. ICK1, a cyclin-dependent protein kinase inhibitor from Arabidopsis thaliana interacts with both Cdc2a and CycD3, and its expression is induced by abscisic acid
AUTHORS Wang, H., Qi, Q., Schorr, P., Cutler, A. J., Crosby, W. L. and Fowke, L. C.
TITLE ICK1, a cyclin-dependent protein kinase inhibitor from Arabidopsis thaliana interacts with both Cdc2a and CycD3, and its expression is induced by abscisic acid
JOURNAL Plant J. 15 (4), 501-510 (1998)
MEDLINE 98426383
REFERENCE 2 (bases 1 to 1240)
AUTHORS Wang, H.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (21-JUL-1998) Saskatoon Research Centre, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada
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BASE COUNT 406 a 125 c 278 g 431 t
ORIGIN

Query Match 52.9%; Score 349.4; DB 8; Length 1240;
Best Local Similarity 79.8%; Pred. No. 1.8e-59;
Matches 478; Conservative 0; Mismatches 6; Indels 115; Gaps 1;

QY 177 gacgtatcgccgggttacgagaggagcttttgaataatctgagagaggagagaaga 236
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Db 496 GAGTTATTTAGGGGTACGAAGAGGAGCTTTTGAATACTGAGAGAGGAGGAGAAGA 555

QY 237 agaattaagtaaatccatgagaaattattcgcgaatttgaaatcgccggttaagaatc 296
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Db 556 AGAATTAAGTAAATCCATGAGGAATTAATCATCGGAATTTGAATCGCGGTTAAAGAATC 615

QY 297 gttagattgtttgttagcgggaggaacacgatggagagacggtgacgcgagagaaga 356
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Db 616 GTTAGATTGTTGTTAGCGGAGGAGAAACGATGGAGAGACCGGTGACGCGGAGGAGGA 675

QY 357 ggagaaggcgaattgatgacgagatgccaacggaatcggaatgaagatttttgt 416
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Db 676 GGAGAGCGCAAAATTGATGCGGAGATGCCAACGGAATCGGAATTTGAAGATTTTTGT 735

QY 417 ggaagctgagaacaactcaaaagaaaattcaagaagaa----- 455
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QY 456 ----- 455

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QY 482 agcaattagaagacgttacgaatgggttaaagttagtggaagaagaagaagtattat 541
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Db 916 AGCCATTAGAAGGCGTTTACGAATGGTAAAGTTAGTGAAGAAGAAGAAGAGTTTAT 975
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Db 1036 TCAATTGGAATAATAAGATTGTAGGAGGAATGTTTITAGAGTACGGAATTCACAGA 1094

RESULT 6
AC003040/c
LOCUS AC003040 98374 bp DNA linear PLN 05-APR-2000
DEFINITION Arabidopsis thaliana chromosome II section 133 of 255 of the complete sequence. Sequence from clones F26B6.
ACCESSION AC003040 AE002093
VERSION AC003040.2 GI:6598387
KEYWORDS HIG.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 98374)
AUTHORS Lin, X., Kaul, S., Rounsley, S. D., Shea, T. P., Benito, M. -I., Town, C. D., Fujii, C. Y., Mason, T. M., Bowman, C. L., Barnstead, M. E., Feldguy, T. V., Buel, C. R., Ketchum, K. A., Lee, J. J., Ronning, C. M., Koo, H., Moffat, K. S., Cronin, L. A., Shen, M., VanAken, S. E., Unayam, L., Tallon, L. J., Gill, J. E., Adams, M. D., Carrera, A. J., Creasy, T. H., Goodman, H. M., Somerville, C. R., Copenhaver, G. P., Preuss, D., Nierman, W. C., White, O., Eisen, J. A., Salzberg, S. L., Fraser, C. M. and Venter, J. C.
TITLE Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
JOURNAL Nature 402 (6763), 761-768 (1999)
MEDLINE 20083487
PUBMED 10617197
REFERENCE 2 (bases 1 to 98374)
AUTHORS Lin, X.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
COMMENT On Dec 17, 1999 this sequence version replaced gi:3242700. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).

Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (http://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are

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predicted by TRNscan-SE (Sean Eddy,
http://genome.wustl.edu/eddy/Trnscan-SE/). Simple repeats were
identified by RepeatMasker (Arian Smit,
http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are
numbered from the top to bottom of the chromosome.

We thank the CSHL/WashU/ABI consortium for sequencing BAC clones
F6p23, F5j6, T17A5, and T13L15, the ESSA group for sequencing clone
F13p4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards
and Satoshi Tabata for helpful assistance. In addition, we would
like to thank the TIGR Bioinformatics Department, especially Lixin
Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy
Peterson, Michael Holmes, and Delwood Richardson for software and
database support.

This work was supported by the National Science Foundation,
Department of Energy and the US Department of Agriculture.

Address all correspondence to: atetigr.org.

```

FEATURES
    source
        1. 98374
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JOURNAL Plant Physiol. 120, 339-339 (1999)
REFERENCE 2 (bases 1 to 804)
AUTHORS Fountain M.D.
TITLE Direct Submission
JOURNAL Submitted (25-NOV-1997) Fountain M.D., Plant Physiology, University of Bayreuth, Universitaetstrasse 30, 95447, GERMANY

FEATURES
source
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BASE COUNT 254 a 151 c 202 g 197 t
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Matches 112; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 354 ggaggagagcggaattgatcgagatgccaacggaatcggaattgaaattgattttt 413
Db 477 GCGCAGCAATCAACGGTACAGATCAAGATCGCGTCGTGATTCAGAAATCGAAGAAATCTT 536

QY 414 ttgtgaagctgagaacaactcaagaaaaattcaagaaagatacaatttcgattcga 473
Db 537 TGCTGTGCTGAAAGAGATCTCCAGAAACGCTTCAGCGAAAGATACATATTCACATAGT 596

QY 474 gaaggagaacccattgaaggagcgttacgaattgggttaaaattgagtgaaagaaga 531
Db 597 TAAGGAGTGCCCACTGAAGAGTCGTATGATGGTTCCTCAATAATCCATGAATAAAA 654

RESULT 12
NT0297906
LOCUS Nicotiana tomentosiformis mRNA for CDK/cyclin inhibitor (kisla gene)
DEFINITION NTO297906 789 bp mRNA linear PLN 03-OCT-2001
ACCESSION AJ297906
VERSION AJ297906.1 GI:15963347
KEYWORDS CDK/cyclin inhibitor; kisla gene.
SOURCE Nicotiana tomentosiformis.
ORGANISM Nicotiana tomentosiformis.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 789)
Grondard S., Perennes C., Bernardi F., Bergounioux C. and Glab N.
The tobacco CDK inhibitor NTKisla is involved in flower development
Unpublished
2 (bases 1 to 789)
Direct Submission
Grondard S.
Submitted (23-OCT-2000) Grondard S., Science de la vie, CNRS, Université, IBP, Université Paris Sud, Bat 630, Orsay, 91405, FRANCE
Location/Qualifiers

JOURNAL Plant Physiol. 120, 339-339 (1999)
REFERENCE 2 (bases 1 to 804)
AUTHORS Fountain M.D.
TITLE Direct Submission
JOURNAL Submitted (25-NOV-1997) Fountain M.D., Plant Physiology, University of Bayreuth, Universitaetstrasse 30, 95447, GERMANY

FEATURES
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Matches 100; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 378 ggagatgccaacggaatcggaattgaaattttttgtggaagctgagaacaactcaa 437
Db 417 GAAATGCCGTCTGAAAAGAGATGAAGATTTTTCAGCTCGCCAGAAAGCTATACT 476

QY 438 agaaaaattcaagaagaagatacaatttcgatttcgagaagaagaccattagaagacg 497
Db 477 TAACGATTTAGAAAAGATCAACTTCGACTTTGAGAAAGAGAGCCATTTGAAGGTCG 536

QY 498 ttacgaatgggttaagttagtgaaagaaga 528
Db 537 CTACGAATGGTCCGATAGGAAAGTTGAAGA 567

RESULT 13
AC091428
LOCUS Mus musculus chromosome 11 clone : MGS1-185K22, MGS1-180K15, MGS1-219p9, MGS1-65111, *** SEQUENCING IN PROGRESS ***, 11
DEFINITION AC091428 286564 bp DNA linear HTG 20-APR-2001
ACCESSION AC091428
VERSION AC091428.1 GI:13699334
KEYWORDS HTG; HTGS_PHASE1; HTGS_FULLTOP.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 286564)
Resch, K., Platzer, M., Fuchs, S., Schilhabel, M., Jockusch, H., Rosenthal, A. and Schmitt-John, T.
Chromosome 11 genomic sequence
Unpublished
2 (bases 1 to 286564)
Platzer, M.
Direct Submission
Submitted (20-APR-2001) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena, Thüringia 07745, Germany
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
* 1 12871: contig of 12871 bp in length

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 30, 2002, 11:42:59 ; Search time 211.8 Seconds
(without alignments)
5350.158 Million cell updates/sec

Title: US-09-733-507-3

Perfect score: 660

Sequence: 1 acgtatgacgtacgag.....gaagtacgaattgcacaga 660

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 176436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.*
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- 22: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	660	100.0	779	21	AA47352
2	660	100.0	904	21	AA229415
3	641.6	97.2	780	21	AA36958
4	72.4	11.0	804	21	AA229420
5	71.6	10.8	470	21	AA02403
6	71.6	10.8	470	21	AA02403
7	63.8	9.7	1341	21	AA33295
8	63	9.5	620	21	AA02401
9	63	9.5	620	21	AA02401

10	61.2	9.3	642	21	AA229418
11	60.4	9.2	870	21	AA095293
12	60.4	9.2	870	21	AA095293
13	58	8.8	467	21	AA095291
14	57.6	8.7	533	21	AA229419
15	57.6	8.7	875	20	AA25016
16	57	8.6	1116	21	AA02402
17	57	8.6	1116	21	AA095288
18	56.6	8.6	621	23	AA090688
19	54.8	8.3	1215	23	AA092075
20	53.6	8.1	1839	22	AA017145
21	53.4	8.1	379	23	AA075428
22	53.4	8.1	379	23	AA090909
23	53.2	8.1	14798	24	ABL33033
24	52.6	8.0	1193	20	AA25017
25	52.4	7.9	575	22	ABA50472
26	52.4	7.9	575	22	ABA68422
27	52.4	7.9	575	22	ABA35413
28	52.4	7.9	575	22	AAK16793
29	52.4	7.9	575	22	AAK42567
30	52.4	7.9	575	22	AAI23315
31	52.4	7.9	575	22	AAI48636
32	52.4	7.9	575	22	AAI08956
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34	52.4	7.9	1969	22	ABA53830
35	52.4	7.9	1969	22	ABA25506
36	52.4	7.9	1969	22	AAK04048
37	52.4	7.9	1969	22	AAK29533
38	52.4	7.9	1969	22	AAI14105
39	52.4	7.9	1969	22	AAI35486
40	52.4	7.9	1969	22	AAI03958
41	52.2	7.9	886	21	AA037798
42	52.2	7.9	932	20	AA25015
43	51.6	7.8	32249	22	ABA17155
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45	51.4	7.8	50000	21	AAA64139

ALIGNMENTS

RESULT 1
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ID AAC47352 standard; DNA; 779 BP.

XX AAC47352;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 53499.

XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EPI033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 08-APR-1999; 99US-0128234.

XX 16-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
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Query Match 100.0%; Score 660; DB 21; Length 779;
Best Local Similarity 100.0%; Pred. No. 2.2e-137;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acgtatcgcagctacgagcgaggaattgtttatgttagatcggaataatcaagctct 60
Db 85 acgtatcgcagctacgagcgaggaattgtttatgttagatcggaataatcaagctct 144

QY 61 gtctccgtcgtcggtgataatggagtttcgtcgtctttagttagtgaagcaatgaataaag 120
Db 145 gtctccgtcgtcggtgataatggagtttcgtcgtctttagttagtgaagcaatgaataaag 204

QY 121 aagaaagaattatcatctgtgaggaagataaagaatgttgacactgaaacgtcgacg 180
Db 205 aagaaagaattatcatctgtgaggaagataaagaatgttgacactgaaacgtcgacg 264

QY 181 taccgaggggtacgaagagaaagctttttgaaatctgagagagggaggaagaagaa 240
Db 265 taccgaggggtacgaagagaaagctttttgaaatctgagagagggaggaagaagaa 324

QY 241 ttaagtaaatccatggagaattattcatcggaatttgaatcgcggttaagaatcggtta 300
Db 325 ttaagtaaatccatggagaattattcatcggaatttgaatcgcggttaagaatcggtta 384

QY 301 gatttgttgttagcggaggaagaaacgatgagagagcggtgacgcgaggagaggag 360
Db 385 gatttgttgttagcggaggaagaaacgatgagagagcggtgacgcgaggagaggag 444

QY 361 aagcgaaattgtagcggagatcccaacggaatcgaaatcgaaatgtttttgtggaa 420
Db 445 aagcgaaattgtagcggagatcccaacggaatcgaaatcgaaatgtttttgtggaa 504

QY 421 gctgagaaacactcaagaaaaattcaagaagaattcaaatctcgatttcgagaaggag 480
Db 505 gctgagaaacactcaagaaaaattcaagaagaattcaaatctcgatttcgagaaggag 564

QY 481 aagcattagaagcgttacgaatgggttaagttagtgaaagaagaagaagttta 540
Db 565 aagcattagaagcgttacgaatgggttaagttagtgaaagaagaagaagttta 624

QY 541 tggtttttttttaacttttagattttatatttcagggaataagttattttttt 600
Db 625 tggtttttttttaacttttagattttatatttcagggaataagttattttttt 684

QY 601 ttgatttggaaataaagattttagaggaagattgtttttagaagtcagaaattgcacaga 660
Db 685 ttgatttggaaataaagattttagaggaagattgtttttagaagtcagaaattgcacaga 744
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RESULT 2
AAZ29415
ID AAZ29415 standard; cDNA; 904 BP.
XX
AC AAZ29415;
XX
DT 29-FEB-2000 (first entry)
XX
DE Arabidopsis thaliana CDK inhibitor, ICK1 encoding cDNA.
XX
KW Cyclin-Dependent kinase inhibitor; CDK; Interactor of Cdc2 kinase 1;
KW ICK1; Cdc2a; D-class cyclin; CycD1; CycD2 and CycD3; morphogenesis;
KW antisense construct; tissue-specific promoter; transgenic plant;
KW male sterility; ds.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 55..630
FT /tag= a
FT /product= "ICK1"
FT /replace (318, G)
FT old_sequence /tag= b
FT /note= "Present in genomic DNA"
FT misc_feature 40..42
FT /tag= c
FT /note= "In-frame stop codon"
FT misc_feature 661..663
FT /tag= d
FT /note= "In-frame stop codon"
XX
PN WO9964599-A1.
XX
PD 16-DEC-1999.
XX
PF 08-JUN-1999; 99WO-CA00532.
XX
PR 08-JUN-1998; 98CA-2235978.
PR 31-DEC-1998; 98CA-2256121.
XX
(MIAC ) AGRIC & AGRIFOOD CANADA.
(PA ) UNIV SASKATCHEWAN TECHNOLOGIES INC.
(PA ) (CANA ) NAT RES COUNCIL CANADA.
XX
Wang H, Fowke LC, Crosby WL;
DR WPI; 2000-097540/08.
DR P-PSDB; AAY44335.
XX
Modifying plant cell development using nucleic acid encoding inhibitor
of cyclin-dependent kinase, or corresponding antisense sequence, e.g.
for inducing male sterility -
Claim 5; Fig 1; 58pp; English.
XX
The present sequence is a cDNA encoding A. thaliana Cyclin-Dependent
kinase (CDK) inhibitor, ICK1. Interactor of Cdc2 kinase 1 (ICK1)
interacts with Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3. Growth,
morphogenesis, multiplication, enlargement, differentiation and
maturation of plant cells can be modified by transforming them with
nucleic acid encoding CDK inhibitor or antisense construct complementary
to the inhibitor gene, operably linked to a tissue-specific promoter.
The transgenic plants exhibit alteration of traits such as petals, male
sterility and ability to set seeds.
XX
Sequence 904 BP; 307 A; 107 C; 229 G; 261 T; 0 other;
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Query Match 100.0%; Score 660; DB 21; Length 904;
Best Local Similarity 100.0%; Pred. No. 2.3e-137;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 601 ttgatttgaaataaagattttagggaggaatttttttagaagacgaataatgcacaga 660
 Db 686 ttgatttgaaataaagattttagggaggaatttttttagaagacgaataatgcacaga 745

RESULT 4
 ID AA229420 standard; cDNA; 804 BP.
 AC AA229420;
 DT 29-FEB-2000 (first entry)
 DE Chenopodium rubrum CDK11 encoding cDNA.
 KW Cyclin-Dependent kinase; CDK; CDK11; Cdc2a; D-class cyclin; CycD1;
 KW CycD2; CycD3; morphogenesis; transgenic plant; male sterility; ds.
 OS Chenopodium rubrum.
 XX Key Location/Qualifiers
 FT CDS 58..648
 FT /*tag= a
 FT /product= "CDK11"
 XX WO9964599-A1.
 PD 16-DEC-1999.
 XX 08-JUN-1999; 99WO-CA00532.
 XX 08-JUN-1998; 98CA-2235978.
 PR 31-DEC-1998; 98CA-2256121.
 XX (MIAC) AGRIC & AGRIFOOD CANADA.
 PA (OISA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
 XX (CANA) NAT RES COUNCIL CANADA.
 PI Wang H, Fowke LC, Crosby WL;
 DR WPI: 2000-097540/08.
 DR P-PSDB; AAY44340.
 XX Modifying plant cell development using nucleic acid encoding inhibitor
 PT of cyclin-dependent kinase, or corresponding antisense sequence, e.g.
 PT for inducing male sterility
 XX Disclosure; Fig 6; 58pp; English.
 PS The present sequence is a cDNA encoding C. rubrum CDK11, which
 CC inhibits Arabidopsis thaliana Cyclin-Dependent kinase (CDK). CDK11
 CC interacts with Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3 and
 CC shares functional and sequence similarity with ICK1. Growth,
 CC morphogenesis, multiplication, enlargement, differentiation and
 CC maturation of plant cells can be modified by transforming them with
 CC Agrobacterium strain harbouring an expression construct of CDK11.
 CC The transgenic plants exhibit alteration of traits such as petals, male
 CC sterility and ability to set seeds.
 XX Sequence 804 BP; 254 A; 151 C; 202 G; 197 T; 0 other;
 SQ

Query Match 11.0%; Score 72.4; DB 21; Length 804;
 Best Local Similarity 62.9%; Pred. No. 7.1e-07;
 Matches 112; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 354 ggagagagagcgaatttagacgagatgcacacggaatcggaattgaatttttt 413
 Db 477 ggcgacgaattcaacggtacagatcaagatgcgctctgattcagaatcggaatttt 536

QY 414 tctggaacttgagaaacactcaagaaattccaagaagaatacattcgatttcga 473
 Db 537 tgcgtgtgctgaaagaagatcccaagaacgcttcagcgaaagatacaatttcgacatagt 596

QY 474 gaagagagcgaatttagacgagatgcacacggaatcggaattgaattgaagaaga 531
 Db 597 taagagcgtgcacactgaaagtcgttatgattgggttccaataataacatgaataaa 654

RESULT 5
 ID AAN02403 standard; DNA; 470 BP.
 AC AAN02403;
 DT 01-NOV-2001 (first entry)
 DE Cyclin dependent kinase inhibitor (CDKI) clone sl2.pk0117.h4.
 KW Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle;
 KW soybean; plant growth inhibitor; ds.
 XX Glycine max.
 XX Key Location/Qualifiers
 FT CDS 2..184
 FT /*tag= a
 FT /product= "CDKI fragment"
 FT /partial
 FT /note= "No start codon given"
 XX WO200060087-A2.
 XX 12-OCT-2000.
 XX 06-APR-2000; 2000WO-US09106.
 XX 07-APR-1999; 99US-0128192.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Klein TM, Weng Z, Cahoon RE;
 DR WPI: 2000-679375/66.
 DR P-PSDB; AAP01953.
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying
 PT herbicides and plant growth inhibitors
 PS Claim 2; Page 51; 58pp; English.
 CC The invention describes a novel isolated polynucleotide comprising a
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in
 CC control of cell division, growth and death. The nucleotide sequences can
 CC be used in a vector to transform a host cell to produce the CDKI
 CC polypeptide. They can also be used in methods for selecting and
 CC obtaining a nucleic acid sequence that encodes CDKI or affects the level
 CC of CDKI expression. The encoded protein can be used in a method for
 CC evaluating a compound for its ability to inhibit the activity of a CDKI.
 CC The inhibitors can be used as herbicides. They can also be used to
 CC inhibit plant growth. The polynucleotide sequences can be used to
 CC mapping and as genetic markers. The sequence encodes the soybean CDKI
 CC clone sl2.pk0117.h4 as described in the method of the invention.
 XX Sequence 470 BP; 155 A; 73 C; 91 G; 151 T; 0 other;
 SQ

Query Match 10.8%; Score 71.6; DB 21; Length 470;
 Best Local Similarity 67.3%; Pred. No. 9.2e-07;
 Matches 101; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 383 tgcaacacgaatcggaattgaatttttttggaagctgagaacaactcaagaaga 442
 Db 42 ttccaacgagctcgagctcgaaagattttctcgtcgtcgcgagaagaacattcagaac 101

QY 443 aattcaagaagaagtacatttcgatttcgagaaaggagaaagccattagaagacgttacg 502
 Db 102 gttcacagacaagtataattatgattttggaagacatgctttggaggacaatacgy 161
 QY 503 aatgggttaaaagttagagtgaaagaagaa 532
 Db 162 agtgggttaaaattgaagtcataaaagtga 191

RESULT 6

AAA95289
 ID AAA95289 standard; cDNA; 470 BP.
 XX
 AC AAA95289;
 XX
 DT 17-JAN-2001 (first entry)
 XX
 DE Soybean cyclin-dependent kinase inhibitor coding sequence #4.
 XX
 KW Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;
 KW CDKI; cell growth; herbicide; ss.
 XX
 OS Glycine max.

PH Key Location/Qualifiers
 FT CDS 2..184
 FT /*tag= a
 FT /product= "CDKI"
 FT /partial

XX W0200060087-A2.

XX 12-OCT-2000.

XX 06-APR-2000; 2000WO-US09106.

XX 07-APR-1999; 99US-0128192.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Klein TM, Weng Z, Cahoon RE;

XX WPI; 2000-679375/66.

XX P-PSDB; AAB27255.

XX Cyclin dependent kinase inhibitor sequences, useful for identifying
 herbicides and plant growth inhibitors

XX Claim 2; Page 51; 58pp; English.

XX The present sequence is the coding sequence for the soybean
 cyclin-dependent kinase inhibitor (CDKI). It was isolated by searching a
 soybean seedling cDNA library for sequences similar to those encoding the
 CDKI from *Chenopodium rubrum*, *Caenorhabditis elegans* and *Arabidopsis*
 thaliana. CDKI is involved in the cell cycle, and may promote or inhibit
 cell division and growth. The coding sequence and the protein it encodes
 are useful in the production of transgenic plants which produce increased
 or decreased amounts of the CDKI protein, in the identification of
 herbicides, in genetic and physical mapping and in the isolation of the
 CDKI gene in other organisms.

XX Sequence 470 BP; 155 A; 73 C; 91 G; 151 T; 0 other;

Query Match 10.8%; Score 71.6; DB 21; Length 470;
 Best Local Similarity 67.3%; Pred. No. 9.2e-07;
 Matches 101; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 383 tgccaacggaatcggaattgaagattttttgtggaagctgagaacaactcaagaaa 442

Db 42 ttccaacggagtcggagctcgaaagattttctctgctgaggagaagacattcagaac 101

QY 443 aattcaagaagaagtacatttcgatttcgagaaaggagaaagccattagaagacgttacg 502

Db 102 gttcacagacaagtataattatgattttggaagacatgctttggaggacaatacgy 161
 QY 503 aatgggttaaaagttagagtgaaagaagaa 532
 Db 162 agtgggttaaaattgaagtcataaaagtga 191

RESULT 7

AAC33295
 ID AAC33295 standard; DNA; 1341 BP.
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 AC AAC33295;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 2504.
 XX
 KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

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XX 08-APR-1999; 99US-0128234.

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XX 28-MAY-1999; 99US-0136392.

XX 01-JUN-1999; 99US-0136782.

XX 03-JUN-1999; 99US-0137222.

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XX 07-JUN-1999; 99US-0137502.

XX 08-JUN-1999; 99US-0137724.

XX 10-JUN-1999; 99US-0138094.

XX 10-JUN-1999; 99US-0138540.

XX 10-JUN-1999; 99US-0138847.

XX 14-JUN-1999; 99US-0139119.

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PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
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XX DT 18-OCT-2000	(first entry)			
XX DE Arabidopsis thaliana	DNA fragment SEQ ID NO: 50239.			
XX KW Hybridisation assay; genetic mapping; gene expression control;				
XX KW protein identification; signal transduction pathway;				
XX KW metabolic pathway; promoter; terminator; termination sequence; ss.				
XX OS Arabidopsis thaliana.				
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XX PD 06-SEP-2000.				
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Query Match
Best Local Similarity 9.2%; Score 60.4; DB 21; Length 870;
Matches 88; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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DT 17-JAN-2001 (first entry)
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KW CDKI; cell growth; herbicide, ss.
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FT /partial
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PN WO2000060087-A2.
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PD 12-OCT-2000.
XX
PE 06-APR-2000; 2000WC-US09106.
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PR 07-APR-1999; 99US-0128192.
XX
(PUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Klein TM, Weng Z, Cahoon RE;
XX
WPI; 2000-679375/66.
XX
P-PSDB; AAB27257.
XX
Cyclin dependent kinase inhibitor sequences, useful for identifying
herbicides and plant growth inhibitors
XX
Claim 2; Page 52; 58pp; English.
XX
The present sequence is the coding sequence for the soybean
cyclin-dependent kinase inhibitor (CDKI). It was isolated by searching a
soybean cDNA library for sequences similar to those encoding the
CDKI from Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis
thaliana. CDKI is involved in the cell cycle, and may promote or inhibit
cell division and growth. The coding sequence and the protein it encodes
are useful in the production of transgenic plants which produce increased
or decreased amounts of the CDKI protein, in the identification of
herbicides, in genetic and physical mapping and in the isolation of the
CDKI gene in other organisms.
XX
SQ Sequence 467 BP; 158 A; 93 C; 95 G; 121 T; 0 other;
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Job time: 307 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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(without alignments)
3447.121 Million cell updates/sec

Title: US-09-733-507-3

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Searched: 383533 seqs, 122816752 residues

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	41.8	6.3	7832	4	Sequence 94, Appl
6	41.8	6.2	1365	1	Sequence 4, Appl
7	41.8	6.2	1365	1	Sequence 4, Appl
8	41.8	6.2	1365	1	Sequence 4, Appl
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10	41.8	6.2	1365	1	Sequence 4, Appl
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12	40.4	6.1	19124	2	Sequence 13, Appl
13	40.4	6.1	51259	3	Sequence 209, App
14	39.8	6.0	10968	2	Sequence 2, Appl
15	39.8	6.0	10968	2	Sequence 2, Appl
16	39.2	5.9	1298	3	Sequence 8, Appl
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18	39.2	5.9	3211	2	Sequence 6, Appl
19	39.2	5.9	3211	2	Sequence 6, Appl
20	39.2	5.9	3901	4	Sequence 2, Appl
21	39.2	5.9	5852	1	Sequence 56, Appl
22	38.8	5.9	243	1	Sequence 74, Appl
23	38.8	5.9	243	1	Sequence 56, Appl
24	38.8	5.9	243	1	Sequence 2, Appl
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28 38.2 5.8 1669 4 US-09-461-697-184
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ALIGNMENTS

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; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

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Sequence 11, Appl
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RESULT 2
US-09-007-005-17
; Sequence 17, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17

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Best Local Similarity 9.8%; Pred. No. 0.0039;  
Matches 24; Conservative 101; Mismatches 120; Indels 0; Gaps 0;
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Qy 208 ttgaaaatctgagaggaggagaagaataagttaaatccattggagaattatto 267
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QY 268 tcggaattgaatcgcggttaagaatacgttagattgttgtagcggagaaaaag 327
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Db 102 nrsnrnsrnsrnsrnsrnsrnsrnsrnsrnsrnsrnsrnsrnsrnsr 161
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QY 328 atggagagacggtgacgcggagagagagagagagagagagagagatgcc 387
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Db 162 nrsnrnsrnsrnsrnsrnsrnsrnsrnsrnsrnsrnsrnsrnsrnsr 221
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QY 388 acggaatcggaattgaagatttttttggaagctgagaaacacaaagaaaattc 447
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Db 222 argcrurgcrgurararcrurcrgcrgcruaagaaaaaagaaaaa 281
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QY 448 aaaaa 452
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Db 282 aaaaa 286

RESULT 3
US-09-244-796-17
; Sequence 17, Application US/09244796
; Patent No. 6281344
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Ribe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350007
; CURRENT APPLICATION NUMBER: US/09/244,796
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17

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[illegible]


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COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,849B
FILING DATE: 1-SEPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5612201man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5355
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1365 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-299-849B-4

Query Match          6.2%; Score 41; DB 1; Length 1365;
Best Local Similarity 50.2%; Pred. No. 0.31;
Matches 101; Conservative 0; Mismatches 100; Indels 0; Gaps

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QY      462 ttctgatctcagaaggagaagccatttagaaggcgtaagtcggtaagttagatg 521
Db       ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1110 GGAAACC CGATGGCTTCACCTTAGCATGCAAGTTCGAAGCC CAGAGAAAGAAAT 1169
QY      522 aagaagaagaagatttatggtttttttttaaccttttagattttaatttcaggga 581
Db       ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1170 GCACAGCGAAGAGTGTTGTTTTTTTCCCCCTTCATTAATTTCTAGTTTTTAGTAA 1229
QY      582 ataagtaaattttatttgtt 602
Db       || |||| ||||| |||||
1230 TCACAAAAATTGATTTGTT 1250

RESULT            8
; Sequence 4, Application US/08142368A
; Patent No. 5925729
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
; APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
; APPLICANT: Lukquin, Christophe; Chomez, Patrick; Traversari, Catia
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof

```


[illegible]

	Db	1230 TCCAGAAAAATTGATTTGGT 1250
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		US-08-037-230D-4
		: Sequence 4, Application US/08037230D
		: Patent No. 6235525
		: GENERAL INFORMATION:
		: APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
		: APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
		: TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
		: TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
		: NUMBER OF SEQUENCES: 30
		: CORRESPONDENCE ADDRESS:
		: ADDRESSEE: Felfe & Lynch
		: STREET: 805 Third Avenue
		: CITY: New York City
		: STATE: New York
		: ZIP: 10022
		: COMPUTER READABLE FORM:
		: MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
		: OPERATING SYSTEM: PC-DOS
		: SOFTWARE: Wordperfect
		: CURRENT APPLICATION DATA:
		: APPLICATION NUMBER: US/08/037,230D
		: CLASSIFICATION: 435
		: PRIOR APPLICATION DATA:
		: APPLICATION NUMBER: PCT/US92/04354
		: FILING DATE: 22-MAY-1992
		: PRIOR APPLICATION DATA:
		: APPLICATION NUMBER: 07/807,043
		: FILING DATE: 12-DECEMBER-1991
		: PRIOR APPLICATION DATA:
		: APPLICATION NUMBER: 07/764,364
		: FILING DATE: 23-SEPTEMBER-1991
		: PRIOR APPLICATION DATA:
		: APPLICATION NUMBER: 07/728,838
		: FILING DATE: 9-JULY-1991
		: PRIOR APPLICATION DATA:
		: APPLICATION NUMBER: 07/705,702
		: FILING DATE: 23-MAY-1991
		: ATTORNEY/AGENT INFORMATION:
		: NAME: Hanson, No. 6235525man D.
		: REGISTRATION NUMBER: 30,946
		: REFERENCE/DOCKET NUMBER: LUD 5353
		: TELECOMMUNICATION INFORMATION:
		: TELEPHONE: (212) 688-9200
		: TELEFAX: (212) 838-3884
		: INFORMATION FOR SEQ ID NO: 4:
		: SEQUENCE CHARACTERISTICS:
		: LENGTH: 1365 base pairs
		: TYPE: nucleic acid
		: STRANDEDNESS: single
		: TOPOLOGY: linear
		: MOLECULE TYPE: genomic DNA
		US-08-037-230D-4
		Query Match 6.2%; Score 41; DB 4; Length 1365;
		Best Local Similarity 50.2%; Pred.No. 0.31;
		Matches 101; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
		QY 402 tgaagatttttggtagctgagaacaaactcaagaataatccaagaagtaca 461
		Db 1050 TGAAGAGGTTCGAATGTAAGAAGCAAGAAAGAGAGAGGAGCGAGGAGGAAAT 1109
		QY 462 ttccgatttcgagaagaaggaccattagaaggaccttacgaatgggttaagttagtg 521
		Db 1110 GGAAAACCCGGATGGTGCTCACCCTTAGGCATGCAGTTGCCAAGCCGAGAAAGAAAT 1169
		QY 522 aagaagaagaagaagttagtggtttttttaacttttttagattttaattcgcaggga 581
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		Db 1230 TCCAGAAAAATTGATTTGGT 1250
		RESULT 11
		US-07-867-106-2/c
		: Sequence 2, Application US/07867106
		: Patent No. 5389526
		: GENERAL INFORMATION:
		: APPLICANT: Slade, Martin B
		: APPLICANT: Chang, Andy C M
		: APPLICANT: Williams, Keith I
		: TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
		: TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
		: NUMBER OF SEQUENCES: 19
		: CORRESPONDENCE ADDRESS:
		: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
		: STREET: One Liberty Place 46th Floor
		: CITY: Philadelphia
		: STATE: PA
		: COUNTRY: USA
		: ZIP: 19103
		: COMPUTER READABLE FORM:
		: MEDIUM TYPE: Floppy disk
		: OPERATING SYSTEM: IBM PC compatible
		: SOFTWARE: PatentIn Release #1.0, Version #1.25
		: CURRENT APPLICATION DATA:
		: APPLICATION NUMBER: US/07/867,106
		: FILING DATE: 19920625
		: PRIOR APPLICATION DATA:
		: APPLICATION NUMBER: AU PJ 7187
		: APPLICATION NUMBER: PCT/AU90/00530
		: FILING DATE: 02-NOV-1989
		: ATTORNEY/AGENT INFORMATION:
		: NAME: Peeney, Joanne Longo
		: REGISTRATION NUMBER: 35,134
		: REFERENCE/DOCKET NUMBER: RICE-0002
		: TELECOMMUNICATION INFORMATION:
		: TELEPHONE: 215-568-3100
		: TELEFAX: 215-568-3439
		: INFORMATION FOR SEQ ID NO: 2:
		: SEQUENCE CHARACTERISTICS:
		: LENGTH: 5852 base pairs
		: TYPE: NUCLEIC ACID
		: STRANDEDNESS: single
		: TOPOLOGY: linear
		: MOLECULE TYPE: DNA (genomic)
		: ANTI-SENSE: NO
		: FEATURE:
		: NAME/KEY: CDS
		: LOCATION: 2378..5038
		: FEATURE:
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		: LOCATION: 2378..5038
		US-07-867-106-2
		Query Match 6.2%; Score 41; DB 1; Length 5852;
		Best Local Similarity 54.2%; Pred.No. 0.52; Mismatches 0; Gaps
		Matches 83; Conservative 0; Indels 70; Indels 0;
		QY 502 gaatyggtaaagtttagtgagaagaagaagtttatggttttttttaactttt 561
		Db 5513 GACGAGATTAAAAACTTAAACAATAAACATATTCATTTTCTTTTCTTTT 5454
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QY 622 tgtaggaggaatgttttttagaagtagcaaatg 654
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Db 5393 TATAAATTTTATATATTTAAATTTTAAAAATTAG 5361

RESULT 12
US-08-487-826B-13/c
; Sequence 13, Application US/0847826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelson, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-487-826B-13

Query Match 6.1%; Score 40.4; DB 2; Length 19124;
Best Local Similarity 55.8%; Pred. No. 1.1;
Matches 77; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 522 aagaagaagaagttatgggttttttttaacttttttagattttaatttcaggga 581
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QY 642 aagtaagaaattgcacag 659
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Db 18287 AATTAGAAATTAAAAAG 18270

RESULT 13

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 30, 2002, 11:42:59 ; Search time 1632.03 Seconds
(without alignments)
5458.227 Million cell updates/sec

Title: US-09-733-507-3

Perfect score: 660

Sequence: 1 acgtatgcagctacggag.....gaagtacgaattgcacaga 660

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST.*

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2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
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7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
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16: em_gss_vrt:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	31.2	352	10	T88456
2	174.6	26.5	329	10	T21659
3	90.4	13.7	1101	12	CNS0039G
4	83.4	12.6	997	12	CNS0059E
5	79	12.0	1101	12	CNS0182P
6	77.8	11.8	987	12	CNS00418
7	74.4	11.3	689	10	BM436399
8	65	9.8	585	10	BG643706
9	63.6	9.6	1201	12	CNS0107R
10	63	9.5	510	10	BI129591
11	62.8	9.5	1101	12	CNS0039G
12	62	9.4	1101	12	CNS0000D1
13	61.8	9.4	1101	12	CNS0106X
14	61	9.2	1101	12	CNS008WC
15	60.6	9.2	623	10	BE347049
16	60	9.1	846	12	CNS008OV
17	59.6	9.0	1101	12	CNS0100X

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21	57.6	8.7	585	12	AZ060400
22	57	8.6	620	10	BE823380
23	56.8	8.6	938	12	CNS006TJ
24	56.8	8.6	1101	12	CNS00F86
25	56.4	8.5	424	10	BI503896
26	56.2	8.5	1067	12	CNS00C08
27	55.2	8.5	1101	12	CNS0006J
28	56	8.5	1030	12	CNS02LP3
29	55.8	8.5	1101	12	CNS010B3
30	55.6	8.4	1204	12	CNS016E2
31	55.2	8.4	555	12	AZ882512
32	55.2	8.4	1206	12	AG052182
33	55	8.3	466	12	AZ296286
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35	55	8.3	928	12	CNS0102F
36	54.8	8.3	548	10	BI510331
37	54.8	8.3	606	10	BI507828
38	54.8	8.3	754	10	BG581898
39	54.8	8.3	766	10	BG581998
40	54.8	8.3	785	10	BG582049
41	54.8	8.3	1101	12	CNS0181N
42	54.6	8.3	671	12	AZ749598
43	54.6	8.3	1201	12	CNS01660
44	54.4	8.2	619	12	AZ221985
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ALIGNMENTS

RESULT 1

T88456
LOCUS 12152 Lambda-PRL2 Arabidopsis thaliana cDNA clone 156J24T7, mRNA
sequence.
T88456
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KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh, L., Ohlrogge,J., Raikhel,N., Somerville,N., Thomashow,M., Retzel, E. and Somerville,C.
Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
95148729
On Apr 14, 1993 this sequence version replaced gi:716808.
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
1. 352
/organism="Arabidopsis thaliana"
/strain="var Columbia"
/db_xref="taxon:3702"
/clone_lib="156J24T7"
/note="Vector: lambda Zip-Lox; Site.1: Sal; Site.2: Not; Lambda PRL2 is a cDNA library derived from equal

quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques). The vector is BRL's lambda zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dt primed cDNA. "

BASE COUNT 112 a 48 c 94 g 84 t 14 others
ORIGIN

Query Match 31.2%; Score 206; DB 10; Length 352;
Best Local Similarity 85.7%; Pred. No. 2.2e-23;

Matches 221; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

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QY 61 gctccgctgctggtgataatggagtttcgctgtctgttctgtttagtggagcaatgaataaag 120
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Db 154 GTCTCCGTCGCGGTGATTAATGGATTTCGCTGCTTCTAGTGGAGCAATGANTATAAG 213
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QY 121 aagaagaatttaatacatctgagaggaagataaagaatggtgacactgaacgtcgagc 180
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Db 214 ANGAAGANTTAATACATCTGGAGGAGAGATTAAGATGGTGACACTGAACGTCGACG 273
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Db 274 TATCGCGGGTACGAGAGGAGAGCTTTTNNAAATCTNTGNCAGAGGTGAANGAG 333
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QY 241 ttaagtaaatccatggag 258
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Db 334 GTTAGTAATCCCTTGGG 351

RESULT 2

T21659
LOCUS 329 bp mRNA linear EST 07-JAN-1998
DEFINITION 3567 Lambda-PRL2 Arabidopsis thaliana cDNA clone 96D1577, mRNA
T21659
ACCESSION
VERSION T21659.1 GI:2757169
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomas, M., Retzel, E. and Somerville, C.
Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
95148729
COMMENT On Jan 7, 1998 this sequence version replaced gi:914567.
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@bm.cl.msu.edu
Seq primer: T7.

FEATURES

Source
1..329
/organism="Arabidopsis thaliana"
/strain="var columbia"
/db_xref="taxon:3702"

/clone="96D1577"

/clone_lib="Lambda-PRL2"

/note="vector: lambda zip-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques). The vector is BRL's lambda zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dt primed cDNA. "

BASE COUNT 106 a 50 c 78 g 82 t 13 others
ORIGIN

Query Match 26.5%; Score 174.6; DB 10; Length 329;
Best Local Similarity 93.7%; Pred. No. 2.1e-18;

Matches 177; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 acgtatatgcagctacgagcggcggaattgtttatgttagatcgaaaaatcaagctct 60
|||||
Db 110 ACGTATATNCAGCTACGAGCGGAGAAATGTTTATGTAGANGGAAAAATCAAGCTCT 169
|||||
QY 61 gctccgctgctggtgataatggagtttcgctgtctgtttagtggagcaatgaataaag 120
|||||
Db 170 GTCTCCGTCGCGGTGATTAATGGGTTTCATCGTCTTCTAGTGGAGCAATGAATNTAAG 229
|||||
QY 121 aagaagaatttaatacatctgagaggaagataaagaatggtgacactgaacgtcgagc 180
|||||
Db 230 NGAAGANTTAATACATCTGGGAGGAGAACTAAAGATGTGTACACATGAACGTCGACG 289
|||||
QY 181 tatcgagcg 189
|||||
Db 290 TATGNCGG 298

RESULT 3

CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
LOCUS CNS0039G/c
DEFINITION Drosophila melanogaster genome survey sequence TBT3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL063921
VERSION AL063921.1 GI:4941778
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).. The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammos in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed in Buffalo, EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers

FEATURES

[illegible]

5

REFERENCE	1 (bases 1 to 1101)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutosyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y ¹ ; cn bw ^{sp} , the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm . Location/Qualifiers 1 1101101
FEATURES	source

[illegible]

RESULT	12
CNS0000D1	
LOCUS	
DEFINITION	CNS0000D1 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC #

BACR01J16 of RCI-98 library from *Drosophila melanogaster* (fruit fly), genomic survey sequence.
AL065414
AL065414.1 GI:4938827
GSS.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; *Drosophila*.
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 131 91006 EVRY cedex - FRANCE (E-mail : seqrf@genoscope.cns.fr - web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley *Drosophila* Genome Project (BDGP). The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org/TheBDGP> melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pictet de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RCI-98 and was constructed by partial, EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at <http://bacpac.med.buffalo.edu/drosophila.bac.htm>.

```

Found at http://acpac.med.utoronto.edu/drosophila_bac.htm.
FEATURES             source
Location/Qualifiers
1. .1101
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACH01J16"
/notes="end : TET3"
BASE COUNT          280 a 104 c 123 g 211 t 383 others
ORIGIN
Query Match          9.4%; Score 62; DB 12; Length 1101;
Best Local Similarity 16.4%; Pred. No. 0.94;
Matches 74; Conservative 207; Mismatches 169; Indels 1; Gaps 1;
QY 170 aaagcgtgcagtcagcagcgggtacgaagaggaagcgttttgaaatctcgaagagagag 229
Db ||| : ||| : : : : ||| : ||| : ||| : : : : ||| : : : : ||| :
593 AAAAAWAGAGATNDDBKADKAAADAKAAAWAGTWWTKKDTKKKKKKKKRGKAK 652
QY 230 agaaagaagaattaaatcatcgatgaggaattattcatcggaatttgaaatcgcggtta 289
Db ||| : ||| : ||| : ||| : : : : ||| : ||| : ||| : ||| : ||| :
653 RAATDDTATATTWTKTAKKADGAKAAKWKADRTKAWKGAGAGCAKATAKARAKRKWD 712
QY 290 aagaatcgttagattgttcttagcggagagaaacgatgagagagacggtgcagcgag 349
Db ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
713 DKTKKKKKYTKTKKKTITTKRAADTKWKKKKKATAGAWDDDDARRRGGWGDKRR 772
QY 350 agagagagagaagcggcaattgatcacgcagatgcacaacggaatcggaattgaagatt 409
Db ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
773 TGARGDKDKTGKKKKTGDKRGKGDDRGDGGAGGDDRDARARARARWDTKTRGAXD 832
QY 410 tttttggaagctgag-aacaacatcaagaagaaattcaagaagaagtacaaatttcgat 468
Db ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
833 KADKKAGRRKKRWTKRWKRTADKAAAWRWRRDRDKDRGRDRWRWRGADKKW 892
QY 469 ttcgagaaggagaagccattaggaagcagcttcaggaatggtaaggttagagtaagaaga 528
Db ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
893 KWDDDDTAKDDWTKDWTAGTAGAWDDDKAKDGDKRGTDWPTWKPWKGWGRKDKG 952
QY 529 aagaagaagttatggttttttttttaacttttttagattttaatttcagggaataagtt 588
Db ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
953 RKTAGRAGDGKKKKGDKDRDADAKDTGKDTWRDITDTAKRRRRRRRAGRGDRKG 1012

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[illegible]

